

Sequence Alignment #2

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<!--StartFragment-->RESULT 2
TSHB_CANFA
ID   TSHB_CANFA                Reviewed;          138 AA.
AC   P54828;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   24-JUL-2007, entry version 40.
DE   Thyrotropin subunit beta precursor (Thyroid-stimulating hormone
DE   subunit beta) (TSH-beta) (TSH-B) (Thyrotropin beta chain).
GN   Name=TSHB;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Pituitary;
RA   Kania S.A., Frank L.A.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Indispensable for the control of thyroid structure and
CC   metabolism.
CC   -!- SUBUNIT: Heterodimer of a common alpha chain and a unique beta
CC   chain which confers biological specificity to thyrotropin,
CC   lutropin, follitropin and gonadotropin.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the glycoprotein hormones subunit beta
CC   family.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; U51644; AAA97410.1; -; mRNA.
DR   UniGene; Cfa.3841; -.
DR   HSSP; P01233; LHCN.
DR   Ensembl; ENSCAFG000000009713; Canis familiaris.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   PANTHER; PTHR11515; Gly_hormoneB; 1.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
PE   2: Evidence at transcript level;
KW   Glycoprotein; Hormone; Secreted; Signal.
FT   SIGNAL          1      20      By similarity.
FT   CHAIN           21     132     Thyrotropin subunit beta.
FT                                     /FTid=PRO_0000011742.
FT   PROPEP          133     138     By similarity.
FT                                     /FTid=PRO_0000011743.
FT   CARBOHYD        43      43      N-linked (GlcNAc . . .) (Potential).
FT   DISULFID        22      72      By similarity.
FT   DISULFID        36      87      By similarity.
FT   DISULFID        39     125      By similarity.
FT   DISULFID        47     103      By similarity.
FT   DISULFID        51     105      By similarity.
FT   DISULFID       108     115      By similarity.
SQ   SEQUENCE   138 AA;  15666 MW;  A3298FFDDF6A005F CRC64;

Query Match          94.5%; Score 728; DB 1; Length 138;
Best Local Similarity 94.9%; Pred. No. 5.7e-65;
Matches 131; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 MTAIYLSVLFLGLACGQAMSFCEPTEYMMHVERKECAYCLTINTTICAGYCMTRDINGKL 60
Db      1 MTAIYLSMLFLGLACGQAMSFCEPTEYTMHVERKECAYCLTINTTICAGYCMTRDINGKL 60

Qy      61 FLPHYALSQDVCTYRDFLYKTVEIPGCPHHVTPYFSYPVAVSCKCGKCNTDYSDCIHEAI 120
Db      61 FLPHYALSQDVCTYRDFMYKTVEIPGCPRHVTPYFSYPVAVSCKCGKCNTDYSDCIHEAI 120

Qy      121 KTDCTKPQKSDVVGVS I 138
Db      121 KTNCTKPQKSYVVGFS I 138
<!--EndFragment-->

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